

Supplementary Material

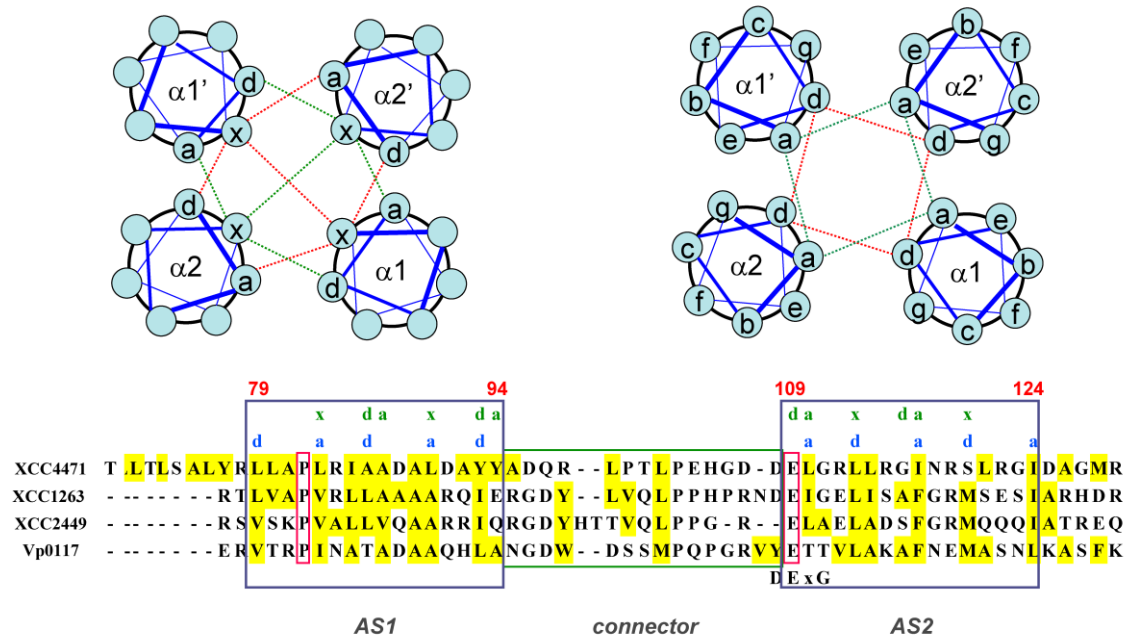


Fig. S1. Helix bundle packing arrangements and sequence alignment of the HAMP domains in GGDEF domain proteins. Top figures show the schematic representation of complementary **x-da** packing (left) versus knobs-into-holes packing (right). The interacting hydrophobic layers are colored in red and green dotted lines, respectively. Bottom figure shows the sequence alignment of the HAMP domains from the three GGDEF domain proteins from *Xcc*, XCC4471 (sequence is equal to XC3486 in strain ATCC33919, gi|21232915), XCC1263 (sequence is equal to XC2274 in strain ATCC33919, gi|21231712), and XCC2449 (sequence is equal to XC2536 in strain ATCC33919, gi|77747895), and Vp0117 from the *Vibrio parahaemolyticus* (gi|28805099). Positions forming the **x** and **da** core layers and forming the **a** and **d** core layers are very similar to those published, including the highly conserved Pro82 and Glu109 residues, which are boxed in red. The two amphiphathic helix sequences and the connector sequence are separately boxed.